



## SEQUENCE LISTING

# 6 A

A1

<110> Meyers, Rachael  
Kapeller-Libermann, Rosana  
Silos-Santiago, Immaculada

<120> 18431 AND 32374, NOVEL HUMAN PROTEIN  
KINASE FAMILY MEMBERS AND USES THEREFOR

<130> 381552002700

<140> 09/916,790

<141> 2001-07-27

<150> 60/221,543

<151> 2000-07-28

<160> 37

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2893

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (274)...(1314)

<221> misc\_feature

<222> (1)...(2893)

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| gtccttgac  | cttgcttg   | ggccgaagga | ctgccccctg                  | ggcctgggtc  | cggtgtgccc | 120 |
| cccttctcac | ttgaagacat | gcaggccctg | actctccgca                  | cacttgcccc  | gccagcgacg | 180 |
| tcaccaagc  | acctacgaaa | ctagtcccgg | gagctgggca                  | aaggcaccta  | cggaaggtt  | 240 |
| gatctggtg  | tctacaagg  | cacaggcaca | aaa atg gca                 | ctg aag ttt | gtg aac    | 294 |
|            |            |            | Met Ala Leu Lys Phe Val Asn |             |            |     |
|            |            |            | 1                           | 5           |            |     |

|   |     |
|---|-----|
| aag agc aaa acc aag ctg aag aac ttc cta cgg gag gtg agc atc acc | 342 |
| Lys Ser Lys Thr Lys Leu Lys Asn Phe Leu Arg Glu Val Ser Ile Thr |     |
| 10 15 20  |     |

|   |     |
|---|-----|
| aac agc ctc tcc tcc agc ccc ttc atc atc aag gtc ttt gac gtg gtc | 390 |
| Asn Ser Leu Ser Ser Ser Pro Phe Ile Ile Lys Val Phe Asp Val Val |     |
| 25 30 35  |     |

|   |     |
|---|-----|
| ttt gag aca gag gac tgc tac gtc ttt gcc cag gag tac gca cct gct | 438 |
| Phe Glu Thr Glu Asp Cys Tyr Val Phe Ala Gln Glu Tyr Ala Pro Ala |     |
| 40 45 50 55   |     |

|   |     |
|---|-----|
| ggg gac ctg ttt gac atc atc cct ccc cag gtg ggg ctc cct gag gac | 486 |
|---|-----|

|   |      |
|---|------|
| Gly Asp Leu Phe Asp Ile Ile Pro Pro Gln Val Gly Leu Pro Glu Asp |      |
| 60 65 70  |      |
| acg gtg aag cgc tgt gtg cag cag ctg ggc ctg gcg ctg gac ttc atg | 534  |
| Thr Val Lys Arg Cys Val Gln Gln Leu Gly Leu Ala Leu Asp Phe Met |      |
| 75 80 85  |      |
| cac ggg cgg cag ctg gtg cac cgc gac atc aag ccc gag aac gtg ctg | 582  |
| His Gly Arg Gln Leu Val His Arg Asp Ile Lys Pro Glu Asn Val Leu |      |
| 90 95 100   |      |
| ctg ttc gac cgc gag tgc cgc cgc gta aag ctg gcc gac ttc ggc atg | 630  |
| Leu Phe Asp Arg Glu Cys Arg Arg Val Lys Leu Ala Asp Phe Gly Met |      |
| 105 110 115   |      |
| acg cgc cgc gtg ggc tgc cgc gtc aag cgc gtg agc ggc acc atc cct | 678  |
| Thr Arg Arg Val Gly Cys Arg Val Lys Arg Val Ser Gly Thr Ile Pro |      |
| 120 125 130 135   |      |
| tac acg gcg cct gag gtg tgc cag gcg ggc cgc gcc gac ggg ctg gcg | 726  |
| Tyr Thr Ala Pro Glu Val Cys Gln Ala Gly Arg Ala Asp Gly Leu Ala |      |
| 140 145 150   |      |
| gtg gac acg ggc gtg gac gtg tgg gcc ttc ggc gtg ctc atc ttc tgc | 774  |
| Val Asp Thr Gly Val Asp Val Trp Ala Phe Gly Val Leu Ile Phe Cys |      |
| 155 160 165   |      |
| gtg ctc acc ggc aac ttc ccg tgg gag gcg gcg tcg ggc gcc gac gcc | 822  |
| Val Leu Thr Gly Asn Phe Pro Trp Glu Ala Ala Ser Gly Ala Asp Ala |      |
| 170 175 180   |      |
| ttc ttc gag gag ttc gtg cgc tgg cag cgg ggc cgc ctg ccg ggg ctg | 870  |
| Phe Phe Glu Glu Phe Val Arg Trp Gln Arg Gly Arg Leu Pro Gly Leu |      |
| 185 190 195   |      |
| cct tcg cag tgg cgc cgc ttc acc gag ccc gcg ctg cgc atg ttc cag | 918  |
| Pro Ser Gln Trp Arg Arg Phe Thr Glu Pro Ala Leu Arg Met Phe Gln |      |
| 200 205 210 215   |      |
| cgc tta ctg gcc ctg gag ccc gag cgc cgc ggc cca gcc aag gag gtg | 966  |
| Arg Leu Leu Ala Leu Glu Pro Glu Arg Arg Gly Pro Ala Lys Glu Val |      |
| 220 225 230   |      |
| ttc cgc ttc ctc aag cac gag ctc acg tcc gag ctg cgc cgc cgg ccc | 1014 |
| Phe Arg Phe Leu Lys His Glu Leu Thr Ser Glu Leu Arg Arg Arg Pro |      |
| 235 240 245   |      |
| tcg cac cgc gcg cgc aag ccc ccc ggg gac cgc ccg ccc gcc gcc ggg | 1062 |
| Ser His Arg Ala Arg Lys Pro Pro Gly Asp Arg Pro Pro Ala Ala Gly |      |
| 250 255 260   |      |
| cca ctg cgc ctc gag gcg cct ggg ccg ctc aag cgg acg gtg ctg acc | 1110 |
| Pro Leu Arg Leu Glu Ala Pro Gly Pro Leu Lys Arg Thr Val Leu Thr |      |
| 265 270 275   |      |
| gag agc ggc agc ggc tcc cgg ccc gcg ccc ccc gcc gtc ggg tcg gtg | 1158 |
| Glu Ser Gly Ser Gly Ser Arg Pro Ala Pro Pro Ala Val Gly Ser Val |      |

| 280                                  | 285                               | 290 | 295 |      |
|--------------------------------------|-----------------------------------|-----|-----|------|
| ccc ttg ccc gtg ccg gtg ccg gtg      | cca gtg ccc gtg ccg gtg cct gtg   |     |     | 1206 |
| Pro Leu Pro Val Pro Val Pro Val      | Pro Val Pro Val Pro Val Pro Val   |     |     |      |
| 300                                  | 305                               | 310 |     |      |
| ccc gag ccc ggc cta gct ccc cag      | ggg ccc ccc ggc cgg acc gac ggc   |     |     | 1254 |
| Pro Glu Pro Gly Leu Ala Pro Gln      | Gly Pro Pro Gly Arg Thr Asp Gly   |     |     |      |
| 315                                  | 320                               | 325 |     |      |
| cgc gcg gac aag agc aaa ggg cag      | gtg gtg ctg gcc acg gcc atc gag   |     |     | 1302 |
| Arg Ala Asp Lys Ser Lys Gly Gln      | Val Val Leu Ala Thr Ala Ile Glu   |     |     |      |
| 330                                  | 335                               | 340 |     |      |
| atc tgc gtc tga gtcgcctccg ccgcctccg | acccggggagc agcccggggc            |     |     | 1354 |
| Ile Cys Val *                        |                                   |     |     |      |
| 345                                  |                                   |     |     |      |
| cgccccgagc cgggtgcccgg tgcggcggtg    | gggaatggag ccacctcgcc gcggggcagg  |     |     | 1414 |
| gggcgcagcg gtgactagg caggacgcgg      | cccggcacct ggtccgtccc cggcgggctg  |     |     | 1474 |
| gtgagggggc caccaaagac ccctagcgcg     | gcctgggtgag cgggggcttg gccagagga  |     |     | 1534 |
| gccaagccgc acagaccga gaattcggag      | gccaccacac aacacacaca cacacacata  |     |     | 1594 |
| cacacacaca cacacacacg ccaggagcaa     | gggagctttc gggccacact cccagacgcc  |     |     | 1654 |
| tccctgagcc ctggaaccgg gactcgttgc     | tcttggcctt ccataccccc tggcagatca  |     |     | 1714 |
| tcttgcggtc ccaccccaga tcccctcctc     | ctcgccatcc cattctgccc cctccccacc  |     |     | 1774 |
| ctgggtacag aaagggactg aagtgttggg     | cagagagggg gcttaaggcc cctgggcaca  |     |     | 1834 |
| ggctgggatc agggcagtg gcaagggca       | gctgtgtcct gcccttcctt ctggaggctg  |     |     | 1894 |
| gaggggagag gccaagccct tggaaaatgt     | agcaaagtgc tgggrwgtcg cataagtgcg  |     |     | 1954 |
| tgtatgtgcg ggacaggccc cgagaagcta     | gtgactcctg cacaccccca ttgcacaaat  |     |     | 2014 |
| gaaatcacag ccaggaggg agggtagctt      | ggcactggct gagaaataga gctctctccc  |     |     | 2074 |
| cgcccctccc cctaaccaca agggattgtc     | ctgacaactt gtggggatag aagggtcac   |     |     | 2134 |
| agggcagggg tctcagctgc ccccatcctt     | agggcagggg agttagtgtg gagccgagag  |     |     | 2194 |
| cagggtcccag ctcccctgc cagccgcact     | gtcccaggcc cagggacctc tgcggggtcc  |     |     | 2254 |
| tcccagccct tgccacacag cctagacgta     | gtagcctggg cttccagcag gtggcgagct  |     |     | 2314 |
| ggttcgtgct ggaaatttct cctgggtttc     | ttgggggtcaa acatgccaac ctccaagacc |     |     | 2374 |
| ccatcctcac gtctccact tttctggcgc      | tggagtgtgc agggcgtagg acctgcatgt  |     |     | 2434 |
| gtgggtgtga gaatgggggc cgggtggacac    | cagggggcga gtgtgtgact aggtgtgtgt  |     |     | 2494 |
| gcacatgtgt aggggtgcaga cgcattgggtg   | ccatcctttg cnttcaatga ctgtgcgtcc  |     |     | 2554 |
| agaccccaaa aaagcggccc ccccaccaca     | ccctgntcct cccaggcagc tgtcccaggg  |     |     | 2614 |
| cgcccaggcc tgccttgac cacagccctc      | aggaaatccg gcaaggaggc cctgcagg    |     |     | 2674 |
| tggttcangc ccaggtagca aaacagagac     | aacagcagcc ccgcctgacc ccctgccct   |     |     | 2734 |
| ntctgtggag gcccgggacc cccgcaataa     | gcaccacatg ggtgaggctg tccctgtcag  |     |     | 2794 |
| ggnccctgc cagggtccct cctgggggtt      | tgggccattt gaggggctct ttgatggg    |     |     | 2854 |
| aggccngcca gagtgaactc cgagcacttt     | ctggctggt                         |     |     | 2893 |

<210> 2

<211> 346

<212> PRT

<213> Homo sapiens

<400> 2

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| Met | Ala | Leu | Lys | Phe | Val | Asn | Lys | Ser | Lys | Thr | Lys | Leu | Lys | Asn | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Arg | Glu | Val | Ser | Ile | Thr | Asn | Ser | Leu | Ser | Ser | Ser | Pro | Phe | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Lys | Val | Phe | Asp | Val | Val | Phe | Glu | Thr | Glu | Asp | Cys | Tyr | Val | Phe |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Ala Gln Glu Tyr Ala Pro Ala Gly Asp Leu Phe Asp Ile Ile Pro Pro  
 50 55 60  
 Gln Val Gly Leu Pro Glu Asp Thr Val Lys Arg Cys Val Gln Gln Leu  
 65 70 75 80  
 Gly Leu Ala Leu Asp Phe Met His Gly Arg Gln Leu Val His Arg Asp  
 85 90 95  
 Ile Lys Pro Glu Asn Val Leu Leu Phe Asp Arg Glu Cys Arg Arg Val  
 100 105 110  
 Lys Leu Ala Asp Phe Gly Met Thr Arg Arg Val Gly Cys Arg Val Lys  
 115 120 125  
 Arg Val Ser Gly Thr Ile Pro Tyr Thr Ala Pro Glu Val Cys Gln Ala  
 130 135 140  
 Gly Arg Ala Asp Gly Leu Ala Val Asp Thr Gly Val Asp Val Trp Ala  
 145 150 155 160  
 Phe Gly Val Leu Ile Phe Cys Val Leu Thr Gly Asn Phe Pro Trp Glu  
 165 170 175  
 Ala Ala Ser Gly Ala Asp Ala Phe Phe Glu Glu Phe Val Arg Trp Gln  
 180 185 190  
 Arg Gly Arg Leu Pro Gly Leu Pro Ser Gln Trp Arg Arg Phe Thr Glu  
 195 200 205  
 Pro Ala Leu Arg Met Phe Gln Arg Leu Leu Ala Leu Glu Pro Glu Arg  
 210 215 220  
 Arg Gly Pro Ala Lys Glu Val Phe Arg Phe Leu Lys His Glu Leu Thr  
 225 230 235 240  
 Ser Glu Leu Arg Arg Arg Pro Ser His Arg Ala Arg Lys Pro Pro Gly  
 245 250 255  
 Asp Arg Pro Pro Ala Ala Gly Pro Leu Arg Leu Glu Ala Pro Gly Pro  
 260 265 270  
 Leu Lys Arg Thr Val Leu Thr Glu Ser Gly Ser Gly Ser Arg Pro Ala  
 275 280 285  
 Pro Pro Ala Val Gly Ser Val Pro Leu Pro Val Pro Val Pro Val Pro  
 290 295 300  
 Val Pro Val Pro Val Pro Val Pro Glu Pro Gly Leu Ala Pro Gln Gly  
 305 310 315 320  
 Pro Pro Gly Arg Thr Asp Gly Arg Ala Asp Lys Ser Lys Gly Gln Val  
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 Val Leu Ala Thr Ala Ile Glu Ile Cys Val  
 340 345

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 gagacagagg actgctacgt ctttgcccag gagtacgcac ctgctgggga cctgtttgac 180  
 atcatccctc cccaggtggg gctccctgag gacacggtga agcgctgtgt gcagcagctg 240  
 ggcttgccgc tggacttcat gcacgggccc cagctggtgc accgcgacat caagcccagag 300  
 aacgtgctgc tgttcgaccg cgagtgccgc cgcgtaaagc tggccgactt cggcatgacg 360  
 cgccgcgtgg gctgccgcgt caagcgcgtg agcggcacca tcccttacac ggccgctgag 420  
 gtgtgccagg cgggcccgcgc cgacgggctg gcggtggaca cgggctgga cgtgtgggccc 480  
 ttcggcgtgc tcatcttctg cgtgctcacc ggcaacttcc cgtgggaggg ggcgtcgggc 540  
 gccgacgcct tcttcgagga gttcgtgcgc tggcagcggg gccgcctgcc ggggctgcct 600  
 tcgcagtggc gccgcttcac cgagcccgcg ctgcgcgtgt tccagcgctt actggccctg 660  
 gagcccagag gccgcggccc agccaaggag gtgttccgct tcctcaagca cgagctcacg 720

|  |      |
|--|------|
| tccgagctgc gccgcgggcc ctgcgaccgc gcgcgcaagc ccccgggga ccgccccccc   | 780  |
| gccgcggggc cactgcgcct cgaggcgctt gggccgctca agcggacggt gctgaccgag  | 840  |
| agcggcagcg gctccccggc cgcgcccccc gccgtcgggt cggtgccctt gccgtgccg   | 900  |
| gtgccggtgc cagtgcctgt gccggtgcct gtgcccagc cgggcctagc tccccagggg   | 960  |
| ccccccggcc ggaccgacgg ccgcgcggac aagagcaaag ggcaggtggt gctggccacg  | 1020 |
| gccatcgaga tctgcgtctg a  | 1041 |
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| ttccctcacc cagtattttc aatcgacccc ccccgctccc cccgcacctc tttctctctc  | 120  |
| gctatatgtc ctttcgtggc cagtttgggc aaggggaagg acaccacaag tcgggggtctt | 180  |
| tcctcagcgt tgggtcgcgg tggctgtgag ggcggaagaa aaggccaggc tgaggggagg  | 240  |
| gtagaggggtg aaaagctcgg atctgtgttt ggggaaggcc aggcttgccg tcctcgccgg | 300  |
| gttccgcgaa ggtaacctt ggctgacttg gctcgcgagc aaagggcagc gtctgagctc   | 360  |
| ccggcgttcc aggagtggcc tctttttag tagcacctga aatgcagcgt ctggtgcact   | 420  |
| aagccgtagc ggcagcagca gccacagcga cagcgtggg gccctgtgta gaagctccat   | 480  |
| cccccttgct tttgtgcttg cctgcgtccc cagactcaga gattatctta gaagacctag  | 540  |
| gactccaaaa atg ttt ccc ctg aag gac gct gaa atg gga gcc ttt acc     | 589  |
| Met Phe Pro Leu Lys Asp Ala Glu Met Gly Ala Phe Thr                |      |
| 1 5 10   |      |
| ttc ttt gcc tcg gct ctg cca cat gat gtt tgt gga agc aat gga ctt    | 637  |
| Phe Phe Ala Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu    |      |
| 15 20 25   |      |
| cct ctc aca cca aat tcc atc aaa att tta ggg cgc ttt caa atc ctt    | 685  |
| Pro Leu Thr Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu    |      |
| 30 35 40 45  |      |
| aaa acc atc acc cat ccc aga ctc tgc cag tat gtg gat att tct agg    | 733  |
| Lys Thr Ile Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg    |      |
| 50 55 60   |      |
| gga aag cat gaa cga cta gtg gtc gtg gct gaa cat tgt gaa cgt agt    | 781  |
| Gly Lys His Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser    |      |
| 65 70 75   |      |
| ctg gaa gac ttg ctt cga gaa agg aaa cct gtg agc tgt tca acg gtt    | 829  |
| Leu Glu Asp Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val    |      |
| 80 85 90   |      |
| ttg tgt ata gca ttt gag gtt ctt cag ggc ttg cag tat atg aac aaa    | 877  |
| Leu Cys Ile Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys    |      |
| 95 100 105   |      |
| cat ggt ata gta cac agg gca ttg tct cct cat aat atc ctg ttg gac    | 925  |
| His Gly Ile Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp    |      |
| 110 115 120 125  |      |

|   |      |
|---|------|
| cga aag gga cat att aaa ttg gct aaa ttt gga ctt tat cac atg aca<br>Arg Lys Gly His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr<br>130 135 140     | 973  |
| gct cat ggt gat gat gtt gat ttc cca ata ggg tat ccc tcg tac ttg<br>Ala His Gly Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu<br>145 150 155     | 1021 |
| gcc cct gag gta att gca cag gga att ttc aaa acc act gat cac atg<br>Ala Pro Glu Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met<br>160 165 170     | 1069 |
| cca agt aaa aaa cca ttg cct tct ggc ccc aaa tca gat gta tgg tct<br>Pro Ser Lys Lys Pro Leu Pro Ser Gly Pro Lys Ser Asp Val Trp Ser<br>175 180 185     | 1117 |
| ctt gga atc att tta ttt gag ctt tgt gtg gga aga aaa tta ttt cag<br>Leu Gly Ile Ile Leu Phe Glu Leu Cys Val Gly Arg Lys Leu Phe Gln<br>190 195 200 205 | 1165 |
| agc ttg gat att tct gaa aga cta aaa ttt ttg ctt act ttg gat tgt<br>Ser Leu Asp Ile Ser Glu Arg Leu Lys Phe Leu Leu Thr Leu Asp Cys<br>210 215 220     | 1213 |
| gta gat gac act tta ata gtt ctg gct gaa gag cat ggt tgt ttg gac<br>Val Asp Asp Thr Leu Ile Val Leu Ala Glu Glu His Gly Cys Leu Asp<br>225 230 235     | 1261 |
| att ata aag gag ctt cct gaa act gtg ata gat ctt ttg aat aag tgc<br>Ile Ile Lys Glu Leu Pro Glu Thr Val Ile Asp Leu Leu Asn Lys Cys<br>240 245 250     | 1309 |
| ctt acc ttc cat cct tct aag agg cca acc cca gat gaa tta atg aag<br>Leu Thr Phe His Pro Ser Lys Arg Pro Thr Pro Asp Glu Leu Met Lys<br>255 260 265     | 1357 |
| gac aaa gta ttc agt gag gta tca cct tta tat acc ccc ttt acc aaa<br>Asp Lys Val Phe Ser Glu Val Ser Pro Leu Tyr Thr Pro Phe Thr Lys<br>270 275 280 285 | 1405 |
| cct gcc agt ctg ttt tca tct tct ctg aga tgt gct gat tta act ctg<br>Pro Ala Ser Leu Phe Ser Ser Ser Leu Arg Cys Ala Asp Leu Thr Leu<br>290 295 300     | 1453 |
| cct gag gat atc agt cag ttg tgt aaa gat ata aat aat gat tac ctg<br>Pro Glu Asp Ile Ser Gln Leu Cys Lys Asp Ile Asn Asn Asp Tyr Leu<br>305 310 315     | 1501 |
| gca gaa aga tct att gaa gaa gtg tat tac ctt tgg tgt ttg gct gga<br>Ala Glu Arg Ser Ile Glu Glu Val Tyr Tyr Leu Trp Cys Leu Ala Gly<br>320 325 330     | 1549 |
| ggt gac ttg gag aaa gag ctt gtc aac aag gaa atc att cga tcc aaa<br>Gly Asp Leu Glu Lys Glu Leu Val Asn Lys Glu Ile Ile Arg Ser Lys<br>335 340 345     | 1597 |

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|---|------|
| cca cct atc tgc aca ctc ccc aat ttt ctc ttt gag gat ggt gaa agc<br>Pro Pro Ile Cys Thr Leu Pro Asn Phe Leu Phe Glu Asp Gly Glu Ser<br>350 355 360 365 | 1645 |
| ttt gga caa ggt cga gat aga agc tcg ctt tta gat gat acc act gtg<br>Phe Gly Gln Gly Arg Asp Arg Ser Ser Leu Leu Asp Asp Thr Thr Val<br>370 375 380     | 1693 |
| aca ttg tcg tta tgc cag cta aga aat aga ttg aaa gat gtt ggt gga<br>Thr Leu Ser Leu Cys Gln Leu Arg Asn Arg Leu Lys Asp Val Gly Gly<br>385 390 395     | 1741 |
| gaa gca ttt tac cca tta ctt gaa gat gac cag tct aat tta cct cat<br>Glu Ala Phe Tyr Pro Leu Leu Glu Asp Asp Gln Ser Asn Leu Pro His<br>400 405 410     | 1789 |
| tca aac agc aat aat gag ttg tct gca gct gcc acg ctc cct tta atc<br>Ser Asn Ser Asn Asn Glu Leu Ser Ala Ala Ala Thr Leu Pro Leu Ile<br>415 420 425     | 1837 |
| atc aga gag aag gat aca gag tac caa cta aat aga att att ctc ttc<br>Ile Arg Glu Lys Asp Thr Glu Tyr Gln Leu Asn Arg Ile Ile Leu Phe<br>430 435 440 445 | 1885 |
| gac agg ctg cta aag gct tat cca tat aaa aaa aac caa atc tgg aaa<br>Asp Arg Leu Leu Lys Ala Tyr Pro Tyr Lys Lys Asn Gln Ile Trp Lys<br>450 455 460     | 1933 |
| gaa gca aga gtt gac att cct cct ctt atg aga ggt tta acc tgg gct<br>Glu Ala Arg Val Asp Ile Pro Pro Leu Met Arg Gly Leu Thr Trp Ala<br>465 470 475     | 1981 |
| gct ctt ctg gga gtt gag gga gct att cat gcc aag tac gat gca att<br>Ala Leu Leu Gly Val Glu Gly Ala Ile His Ala Lys Tyr Asp Ala Ile<br>480 485 490     | 2029 |
| gat aaa gac act cca att cct aca gat aga caa att gaa gtg gat att<br>Asp Lys Asp Thr Pro Ile Pro Thr Asp Arg Gln Ile Glu Val Asp Ile<br>495 500 505     | 2077 |
| cct cgc tgt cat cag tac gat gaa ctg tta tca tca cca gaa ggt cat<br>Pro Arg Cys His Gln Tyr Asp Glu Leu Leu Ser Ser Pro Glu Gly His<br>510 515 520 525 | 2125 |
| gca aaa ttt agg cgt gta tta aaa gcc tgg gta gtg tct cat cct gat<br>Ala Lys Phe Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp<br>530 535 540     | 2173 |
| ctt gtg tat tgg caa ggt ctt gac tca ctt tgt gct cca ttc cta tat<br>Leu Val Tyr Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr<br>545 550 555     | 2221 |
| cta aac ttc aat aat gaa gcc ttg gct tat gca tgt atg tct gct ttt<br>Leu Asn Phe Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe<br>560 565 570     | 2269 |
| att ccc aaa tac ctg tat aac ttc ttc tta aaa gac aac tca cat gta   | 2317 |

|   |      |
|---|------|
| Ile Pro Lys Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val<br>575 580 585  |      |
| ata caa gag tat ctg act gtc ttc tct cag atg att gca ttt cat gat<br>Ile Gln Glu Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp<br>590 595 600 605 | 2365 |
| cca gag ctg agt aat cat ctc aat gag att ggt ttc att cca gat ctc<br>Pro Glu Leu Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu<br>610 615 620     | 2413 |
| tat gcc atc cct tgg ttt ctt acc atg ttt act cat gta ttt cca cta<br>Tyr Ala Ile Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu<br>625 630 635     | 2461 |
| cac aaa att ttc cac ctc tgg gat acc tta cta ctt ggg aat tcc tct<br>His Lys Ile Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser<br>640 645 650     | 2509 |
| ttc cca ttc tgt att gga gta gca att ctt cag cag ctg cgg gac cgg<br>Phe Pro Phe Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg<br>655 660 665     | 2557 |
| ctt ttg gct aat ggc ttt aat gag tgt att ctt ctc ttc tcc gat tta<br>Leu Leu Ala Asn Gly Phe Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu<br>670 675 680 685 | 2605 |
| cca gaa att gac att gaa cgc tgt gtg aga gaa tct atc aac ctg ttt<br>Pro Glu Ile Asp Ile Glu Arg Cys Val Arg Glu Ser Ile Asn Leu Phe<br>690 695 700     | 2653 |
| tgt tgg act cct aaa agt gct act tac aga cag cat gct caa cct cca<br>Cys Trp Thr Pro Lys Ser Ala Thr Tyr Arg Gln His Ala Gln Pro Pro<br>705 710 715     | 2701 |
| aag cca tct tct gac agc agt gga ggc aga agt tgc gca cct tat ttc<br>Lys Pro Ser Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe<br>720 725 730     | 2749 |
| tct gct gag tgt cca gat cct cca aag aca gat ctg tca aga gaa tcc<br>Ser Ala Glu Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser<br>735 740 745     | 2797 |
| atc cca tta aat gac ctg aag tca gaa gta tca cca cgg att tca gca<br>Ile Pro Leu Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala<br>750 755 760 765 | 2845 |
| gag gac ctg att gac ttg tgt gag ctc aca gtg aca ggc cac ttc aaa<br>Glu Asp Leu Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys<br>770 775 780     | 2893 |
| aca ccc agc aag aaa aca aag tcc agt aaa cca aag ctc ctg gtg gtt<br>Thr Pro Ser Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val<br>785 790 795     | 2941 |
| gac atc cgg aat agt gaa gac ttt att cgt ggt cac att tca gga agc<br>Asp Ile Arg Asn Ser Glu Asp Phe Ile Arg Gly His Ile Ser Gly Ser<br>2989            |      |



|  |     |     |  |
|--|-----|-----|--|
| 800  | 805 | 810 |  |
| atc aac att cca ttc agt gct gcc ttc act gca gaa ggg gag ctt acc<br>Ile Asn Ile Pro Phe Ser Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr<br>815 820 825  |     |     | 3037   |
| cag ggc cct tac act gct atg ctc cag aac ttc aaa ggg aag gtc att<br>Gln Gly Pro Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile<br>830 835 840 845  |     |     | 3085   |
| gtc atc gtg ggg cat gtg gca aaa cac aca gct gag ttt gca gct cac<br>Val Ile Val Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His<br>850 855 860  |     |     | 3133   |
| ctt gtg aag atg aaa tat cca aga atc tgt att cta gat ggt ggc att<br>Leu Val Lys Met Lys Tyr Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile<br>865 870 875  |     |     | 3181   |
| aat aaa ata aag cca aca ggc ctc ctc acc atc cca tct cct caa ata<br>Asn Lys Ile Lys Pro Thr Gly Leu Leu Thr Ile Pro Ser Pro Gln Ile<br>880 885 890  |     |     | 3229   |
| tga a gaaccaagag tgtgactgcc aaaacttagt gtggcatcag caccaacagc<br>*  |     |     | 3283   |
| acagttcttc atatccacgc cactctcaga caaaactaga tgtccagatt gttgcatttc<br>cgtaaagttt gtcacgagac attttttaaa atctcataac ccacatgttc agttatccat<br>gcaagaaact tgactctaca tgtattgctg aaagaatttt cttaacagtg aaatctgac<br>atatattttt accacactgc cacataaagc ccaagaaatt cagctgacaa gacagattta<br>gcattatcaa gaaatcccat ttgccctgaa aaagctgtcc tccattgtac tgaacagaca<br>gtcctgtcga ttgtgttatt tagaaacata cactgaatgt gggctgaaat catcatcttt<br>ccataatgaa aactgagaaa ctattcacia tgcattcctt ataaataaat gctacattta<br>gtaactcatt tcacccaaac aagaaagatg tgtgtgtgtg tgtgtatagg aagtggagtt<br>tatccccatt gcagaaagtg gtaatactta ctcccagaaa aatgaaattt agaaaccatt<br>tatatttgat agaatttttg gtcagttcct gtagcaaaga cgaatggctt aaacaaattt<br>tctagtttct ttatcacatg aaagtctgta cagtcagtc agggctagtc tactggtttc<br>ctgatcatta agaactcatt accttctctc attgctttac aaacctcaat atgtggcatc<br>catctcatgg atgaaaatgg ctctcagct tctaccatca catctgctat ctagaaggaa<br>gagaatgagg gaaggaggga ggggatgaag agaaaagaag gaacaaaaaa aaaaaaaa<br>aaaaaaaaaaa aaa |     |     | 3343<br>3403<br>3463<br>3523<br>3583<br>3643<br>3703<br>3763<br>3823<br>3883<br>3943<br>4003<br>4063<br>4123<br>4136 |
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| <213> Homo sapiens   |     |     |  |
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 Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys His Gly Ile  
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 Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp Arg Lys Gly  
 115 120 125  
 His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr Ala His Gly  
 130 135 140  
 Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu Ala Pro Glu  
 145 150 155 160  
 Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met Pro Ser Lys  
 165 170 175  
 Lys Pro Leu Pro Ser Gly Pro Lys Ser Asp Val Trp Ser Leu Gly Ile  
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 Thr Leu Ile Val Leu Ala Glu Glu His Gly Cys Leu Asp Ile Ile Lys  
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 Glu Leu Pro Glu Thr Val Ile Asp Leu Leu Asn Lys Cys Leu Thr Phe  
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 His Pro Ser Lys Arg Pro Thr Pro Asp Glu Leu Met Lys Asp Lys Val  
 260 265 270  
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 Ser Ile Glu Glu Val Tyr Tyr Leu Trp Cys Leu Ala Gly Gly Asp Leu  
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 Glu Lys Glu Leu Val Asn Lys Glu Ile Ile Arg Ser Lys Pro Pro Ile  
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 Cys Thr Leu Pro Asn Phe Leu Phe Glu Asp Gly Glu Ser Phe Gly Gln  
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 Gly Arg Asp Arg Ser Ser Leu Leu Asp Asp Thr Thr Val Thr Leu Ser  
 370 375 380  
 Leu Cys Gln Leu Arg Asn Arg Leu Lys Asp Val Gly Gly Glu Ala Phe  
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 Tyr Pro Leu Leu Glu Asp Asp Gln Ser Asn Leu Pro His Ser Asn Ser  
 405 410 415  
 Asn Asn Glu Leu Ser Ala Ala Ala Thr Leu Pro Leu Ile Ile Arg Glu  
 420 425 430  
 Lys Asp Thr Glu Tyr Gln Leu Asn Arg Ile Ile Leu Phe Asp Arg Leu  
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 450 455 460  
 Val Asp Ile Pro Pro Leu Met Arg Gly Leu Thr Trp Ala Ala Leu Leu  
 465 470 475 480  
 Gly Val Glu Gly Ala Ile His Ala Lys Tyr Asp Ala Ile Asp Lys Asp  
 485 490 495  
 Thr Pro Ile Pro Thr Asp Arg Gln Ile Glu Val Asp Ile Pro Arg Cys  
 500 505 510  
 His Gln Tyr Asp Glu Leu Leu Ser Ser Pro Glu Gly His Ala Lys Phe  
 515 520 525

Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr  
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 Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe  
 545 550 555 560  
 Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys  
 565 570 575  
 Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu  
 580 585 590  
 Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu  
 595 600 605  
 Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile  
 610 615 620  
 Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile  
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 Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe  
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 Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg Leu Leu Ala  
 660 665 670  
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 Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu  
 725 730 735  
 Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu  
 740 745 750  
 Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu  
 755 760 765  
 Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser  
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 Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val Asp Ile Arg  
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 Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val  
 835 840 845  
 Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys  
 850 855 860  
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| catgatgttt | gtggaagcaa | tggacttcct  | ctcacaccaa | attccatcaa | aattttaggg  | 120 |
| cgctttcaaa | tccttaaaac | catcacccat  | cccagactct | gccagtatgt | ggatatttct  | 180 |
| aggggaaagc | atgaacgact | agtggctcgtg | gctgaacatt | gtgaacgtag | tctggaagac  | 240 |

|             |             |             |             |             |             |      |
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| ttgcttcgag  | aaaggaaacc  | tgtgagctgt  | tcaacggttt  | tgtgtatagc  | atttgaggtt  | 300  |
| cttcaggggt  | tgcagtatat  | gaacaaacat  | ggtatagtag  | acagggcatt  | gtctcctcat  | 360  |
| aatatcctgt  | tggaccgaaa  | gggacatatt  | aaattggcta  | aatttggact  | ttatcacatg  | 420  |
| acagctcatg  | gtgatgatgt  | tgatttccca  | ataggggtatc | cctcgtactt  | ggcccctgag  | 480  |
| gtaattgcac  | aggggaatttt | caaaaccact  | gatcacatgc  | caagtaaaaa  | accattgcct  | 540  |
| tctggcccca  | aatcagatgt  | atgggtctctt | ggaatcattt  | tatttgagct  | ttgtgtggga  | 600  |
| agaaaattat  | ttcagagctt  | ggatatttct  | gaaagactaa  | aatttttgct  | tactttggat  | 660  |
| tgtgtagatg  | acactttaat  | agttctggct  | gaagagcatg  | gttgtttgga  | cattataaag  | 720  |
| gagcttcctg  | aaactgtgat  | agatcttttg  | aataagtgcc  | ttaccttcca  | tccttctaag  | 780  |
| aggccaaccc  | cagatgaatt  | aatgaaggac  | aaagtattca  | gtgaggtatc  | acctttatat  | 840  |
| acccccctta  | ccaaacctgc  | cagtctgttt  | tcactctctc  | tgagatgtgc  | tgatttaact  | 900  |
| ctgcctgagg  | atatcagtca  | gttggtgtaa  | gatataaata  | atgattacct  | ggcagaaaga  | 960  |
| tctattgaag  | aagtgtatta  | cctttgggtg  | ttggctggag  | gtgacttgga  | gaaagagctt  | 1020 |
| gtcaacaagg  | aaatcattcg  | atccaaacca  | cctatctgca  | cactcccaaa  | ttttctcttt  | 1080 |
| gaggatgggtg | aaagcttttg  | acaaggctga  | gatagaagct  | cgctttttaga | tgataccact  | 1140 |
| gtgacattgt  | cgttatgcc   | gctaagaaat  | agattgaaag  | atgttgggtg  | agaagcattt  | 1200 |
| tacccattac  | ttgaagatga  | ccagtcta    | ttacctcatt  | caaacagcaa  | taatgagttg  | 1260 |
| tctgcagctg  | ccacgctccc  | tttaatcatc  | agagagaagg  | atacagagta  | ccaactaaat  | 1320 |
| agaattattc  | tcttcgacag  | gctgctaaag  | gcttatccat  | ataaaaaaaa  | ccaaatctgg  | 1380 |
| aaagaagcaa  | gagttgacat  | tcctcctctt  | atgagaggtt  | taacctgggc  | tgctctcttg  | 1440 |
| ggagttgagg  | gagctattca  | tgccaagtac  | gatgcaattg  | ataaagacac  | tccaattcct  | 1500 |
| acagatagac  | aaattgaagt  | ggatattcct  | cgctgtcatc  | agtacgatga  | actgttatca  | 1560 |
| tcaccagaag  | gtcatgcaaa  | atttaggcgt  | gtattaaaag  | cctgggtagt  | gtctcatcct  | 1620 |
| gatcttgtgt  | attggcaagg  | tcttgactca  | ccttggtgctc | cattcctata  | tctaaacttc  | 1680 |
| aataatgaag  | ccttggtcta  | tgcatgtatg  | tctgctttta  | ttcccaaata  | cctgtataac  | 1740 |
| ttcttcttaa  | aagacaactc  | acatgtaata  | caagagtatc  | tgactgtctt  | ctctcagatg  | 1800 |
| attgcatttc  | atgatccaga  | gctgagta    | catctcaatg  | agattgggtt  | cattccagat  | 1860 |
| ctctatgcc   | tcccttggtt  | tcttaccatg  | tttactcatg  | tatttccact  | acacaaaatt  | 1920 |
| ttccacctct  | gggatacctt  | actacttggg  | aattcctctt  | tcccattctg  | tattggagta  | 1980 |
| gcaattcttc  | agcagctgcg  | ggaccggcct  | ttggctaagt  | gctttaatga  | gtgtattctt  | 2040 |
| ctcttctccg  | atttaccaga  | aattgacatt  | gaacgctgtg  | tgagagaatc  | tatcaacctg  | 2100 |
| ttttgttgga  | ctcctaaaag  | tgctacttac  | agacagcatg  | ctcaacctcc  | aaagccatct  | 2160 |
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| ccaaagacag  | atctgtcaag  | agaatccatc  | ccattaaatg  | acctgaagtc  | agaagtatca  | 2280 |
| ccacggattt  | cagcagagga  | cctgattgac  | ttgtgtgagc  | tcacagtgac  | aggccacttc  | 2340 |
| aaaacaccca  | gcaagaaaac  | aaagtcagat  | aaaccaaagc  | tcctgggtgg  | tgacatccgg  | 2400 |
| aatagtgaag  | actttattcg  | tggtcacatt  | tcaggaagca  | tcaacattcc  | attcagtgct  | 2460 |
| gccttcactg  | cagaagggga  | gcttaccag   | ggccttaca   | ctgctatgct  | ccagaacttc  | 2520 |
| aaaggggaagg | tcattgtcat  | cgtggggcat  | gtggcaaaac  | acacagctga  | gtttgcagct  | 2580 |
| caccttgtga  | agatgaaata  | tccaagaatc  | tgtattctag  | atgggtggcat | taataaaaata | 2640 |
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<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 7

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| Val | Ala | Val | Lys | Ile | Leu | Lys | Lys | Glu | Ser | Leu | Ser | Leu | Arg | Glu | Ile |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Ile | Leu | Lys | Arg | Leu | Ser | His | Pro | Asn | Ile | Val | Arg | Leu | Leu | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Val | Phe | Glu | Asp | Thr | Asp | Asp | His | Leu | Tyr | Leu | Val | Met | Glu | Tyr | Met |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser  
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 Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu  
 65 70 75 80  
 Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn  
 85 90 95  
 Ile Leu Leu Asp Glu Asn Gly Thr Val Lys Ile Ala Asp Phe Gly Leu  
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 Ala Arg Leu Leu Glu Lys Leu Thr Thr Phe Val Gly Thr Pro Trp Tyr  
 115 120 125  
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 130 135 140  
 Val Asp Val Trp Ser Leu Gly Val Ile Leu Tyr Glu Leu Leu Thr Gly  
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 Gly Pro Leu Phe Pro Gly Ala Asp Leu Pro Ala Phe Thr Gly Gly Asp  
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 Glu Val Asp Gln Leu Ile Ile Phe Val Leu Lys Leu Pro Phe Ser Asp  
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 Lys Lys Arg Arg Leu Pro Leu Pro Ser Asn Cys Ser Glu Glu Leu Lys  
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 Leu Pro Lys Lys Phe Asn Pro Phe Ser Glu Lys Ala Leu Lys Leu Phe  
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 Met Ala His Ile Val Asp Asp Ile Thr His Tyr Leu Leu Phe Asp Lys  
 35 40 45  
 Tyr Ser Gln Asn Phe Leu Glu Tyr Ile Glu Glu Leu Lys Ile Gly Gly  
 50 55 60  
 Glu Val Asp Glu Leu Lys His Leu Lys Tyr Phe Ser Gly Ile Val Ser  
 65 70 75 80  
 Ala Ile Glu Gln Leu His Gly Phe Glu Phe Ala His Leu Asp Ile Lys  
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 Pro Ala Asn Ile Leu Lys Ser Gly Asp Thr Ile Lys Met Ile Asp Phe  
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<400> 12

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 Leu Lys Asp Met Leu Ser Ile Leu Tyr Gln Val Ser Gln Ala Leu Lys  
 35 40 45  
 Tyr Ile His Ser Gln Leu Asp Glu Phe Gly Gln Glu Leu Thr His Gly  
 50 55 60  
 Arg Ile Phe Thr Arg Asn Val Leu Val Thr Glu Pro Asp Leu Arg Lys  
 65 70 75 80  
 Cys Glu Val Lys Leu Gly Asp Phe Gly Asp Ala Pro Met Gly Leu Glu  
 85 90 95  
 Tyr Ser Thr Pro Ile Ile Ala Tyr Met Pro Pro Glu Ile Leu Cys Cys  
 100 105 110  
 Ala Glu Arg Ile Pro Pro His Arg Pro Glu Asn Asp Val Trp Met Phe  
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 Gly Val Phe Ile Trp Glu Cys Leu Thr Leu Gly Ala Gln Pro  
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<220>  
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 Asp Asp Glu Ile Pro Gln Leu Val Val Ala Asp Phe Gly Cys Ala Leu  
 35 40 45  
 Ala Cys Asp Asn Trp Gln Val Asp Tyr Glu Ser Asp Glu Val Ser Leu  
 50 55 60  
 Gly Gly Asn Ala Lys Thr Lys Ala Pro Glu Ile Ala Thr Ala Val Pro  
 65 70 75 80  
 Gly Lys Asn Val Lys Val Asn Phe Glu Met Ala Asp Thr Trp Ala Ala  
 85 90 95  
 Gly Gly Leu Ser Tyr Glu Val Leu Thr Arg Ser Asn Pro Phe Tyr Lys  
 100 105 110  
 Leu Leu Asp Thr Ala Thr Tyr Gln Glu Ser Glu Leu Pro Ala Leu Pro  
 115 120 125  
 Ser Arg  
 130

<210> 14  
 <211> 196  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 14  
 Leu Pro Val Asp Gln Leu Glu Ala Tyr Gly Asp Tyr Leu Phe Gly Ala

1 5 10 15  
 Val Asp Phe Leu Glu Gly Glu Gly Ile Trp His Arg Asp Ile Lys Pro  
 20 25 30  
 Asp Asn Ile Ala Val Arg Ile Arg Pro Asn Arg Thr Arg Glu Leu Val  
 35 40 45  
 Leu Ile Asp Phe Ser Leu Ala Gly Tyr Pro Ala Lys Asn Thr Asp Ala  
 50 55 60  
 Gly Thr Asp Gly Tyr Leu Asp Pro Phe Val Asp Val Ile Thr Arg Gly  
 65 70 75 80  
 Ser Tyr Asp Ser His Ala Glu Arg Tyr Ala Val Ala Val Thr Leu His  
 85 90 95  
 Gln Met Ala Ser Gly Glu Leu Pro Lys Trp Gly Asp Gly Ser Val Leu  
 100 105 110  
 Pro Arg Met Thr Asp Pro Lys Glu Trp Pro Tyr Pro Thr Ile Ala Ala  
 115 120 125  
 Glu Ala Phe Asp Pro Ala Val Arg Asp Gly Leu Val Ala Phe Phe Gln  
 130 135 140  
 Lys Ala Leu His Arg Asp Ala Gly Lys Arg Phe Pro Glu Leu Lys Pro  
 145 150 155 160  
 Met Arg Asp Ala Trp Arg Lys Val Phe Leu Asp Ala Ser Gln Thr Val  
 165 170 175  
 Pro Ser Ser His Arg Thr Arg Pro Ala Ala Pro Ala Asp Gly Ala Ala  
 180 185 190  
 Pro Ala Glu Gly  
 195

<210> 15

<211> 170

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 15

Pro Gly Ile Leu Ala Ile Glu Asn Val Ser Glu Glu Glu Asp Arg Cys  
 1 5 10 15  
 Phe Leu Val Thr Gln Glu Asn Asp Gly Pro Ile Leu Ser Leu Thr Gln  
 20 25 30  
 Tyr Leu Lys Gly Ile Pro Arg Lys Leu Thr Glu Glu Glu Ile Val Asp  
 35 40 45  
 Ile Ile Gln Gln Leu Cys Ser Leu Leu Asp Tyr Val His Ser Glu Gly  
 50 55 60  
 Leu Ala His Gly Gln Trp Asn Leu His Ser Val His Ile His Phe Leu  
 65 70 75 80  
 Asn Gly Val Pro Asn Ile Tyr Leu Pro Asp Leu Gly Phe Ala Ser Leu  
 85 90 95  
 Ile Arg Glu Arg Met Phe Asp Gly Phe Met Gln Asp Glu Glu Asn Arg  
 100 105 110  
 Glu Ser Ile Glu Lys Ile Arg Asp Arg Leu Leu Phe His Thr Pro Glu  
 115 120 125  
 Gly Lys Gln Thr Asn Gly Arg Glu Thr Asp Thr Tyr Ala Phe Gly Ala  
 130 135 140  
 Ile Thr Tyr Tyr Leu Leu Phe Gly Phe Phe Pro Trp Gly Ile Phe Pro  
 145 150 155 160  
 Lys Pro Ser Lys Cys Phe Pro Asp Phe Ile  
 165 170



<210> 16  
 <211> 215  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 16  
 Ser Pro His Val Leu Pro Val Arg Asp Leu Ile Asp Glu Gly Glu Trp  
 1 5 10 15  
 Leu Ser Leu Val Phe Glu Pro Arg Arg Thr Ile Thr Leu Arg Glu Leu  
 20 25 30  
 Leu Ser Ala Gly Pro Val Ser Pro Glu Leu Leu Gln Pro Leu Thr Thr  
 35 40 45  
 Ala Leu Phe Glu Gly Leu Ser Ala Ala His Gln Gly Ala Leu Leu His  
 50 55 60  
 Thr Gln Ile Ser Pro Glu Ala Val Trp Phe Asp Thr Gln Lys Arg Pro  
 65 70 75 80  
 Leu Leu Ala Glu Phe Gly Leu Ala Arg Arg Thr Ala Gln Glu Leu Arg  
 85 90 95  
 Asp His Trp Pro His Asp Pro Arg Tyr Ala Ala Pro Glu Leu Leu Ser  
 100 105 110  
 Gly Gly Pro Tyr Thr Pro Gln Thr Asp Leu Tyr Ala Leu Ala Ala Thr  
 115 120 125  
 Leu Leu Glu Ala Ala Thr Gly Thr Ala Leu Ser Pro Val Ser Ala Arg  
 130 135 140  
 Gln Gln Gly Val Arg Leu Pro Ser Trp Pro Ala Gly Ile Pro Pro Gln  
 145 150 155 160  
 Val Ala His Ala Leu Glu Ser Cys Leu Gln Leu Asp Pro Ala Val Arg  
 165 170 175  
 Ala Val Ser Ala Ala Glu Val Leu Glu Glu Leu Arg Arg Ala Gln Pro  
 180 185 190  
 Thr Gln Ala Ile Leu Ser Gln Gln Glu Pro Pro Ala Pro Pro Pro Ser  
 195 200 205  
 Val Pro Ser Pro Pro Ala Ala  
 210 215

<210> 17  
 <211> 237  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 17  
 Gln Ile Leu Lys Arg Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly  
 1 5 10 15  
 Val Phe Glu Asp Thr Asp Asp His Leu Tyr Leu Val Met Glu Tyr Met  
 20 25 30  
 Glu Gly Gly Asp Leu Phe Asp Tyr Leu Arg Arg Asn Gly Pro Leu Ser  
 35 40 45  
 Glu Lys Glu Ala Lys Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu  
 50 55 60  
 Tyr Leu His Ser Asn Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn



Leu Asp Glu Ile Asp Glu Glu Gln Ala Phe Trp Cys Leu Val Lys Leu  
 210 215 220  
 Met Asp Asn Tyr Leu Pro Gln Lys Tyr Phe Leu Asn Asp Leu Ser Gly  
 225 230 235 240  
 Leu Asn Glu Asp Leu Arg Val Leu Asp Ser Leu Val Lys Glu Ser Leu  
 245 250 255  
 Pro Glu Leu Tyr Ser His Leu Lys Lys Lys Glu Asn Lys Thr Gly Ser  
 260 265 270  
 Gly Lys Lys Lys Asn Leu Leu Ala Leu Asp Leu Thr Leu Leu Ile Phe  
 275 280 285  
 Ala Phe Pro Trp Phe Leu Thr Leu Phe Ala Arg Glu Leu Pro Leu Glu  
 290 295 300  
 Ile Val Leu Arg Ile Trp Asp Ile Leu Phe Thr Tyr Tyr Leu Gly Ser  
 305 310 315 320  
 His Phe Leu Ile Phe Val Ala Leu Ala Ile Leu Lys Leu Leu Lys Ser  
 325 330 335  
 Lys Leu Leu Lys His  
 340

<210> 19  
 <211> 170  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 19  
 Ile Gln Arg Glu Thr Asn Ile Asp Val Pro Pro Thr Leu Arg Gly Glu  
 1 5 10 15  
 Val Trp Gly Cys Leu Leu Arg Val Pro Pro Ser Ala Arg Thr Arg Tyr  
 20 25 30  
 Ala Leu Leu Asp His Ala Val His His Thr Ala Ala Lys Pro Thr Pro  
 35 40 45  
 His Asp Arg Gln Leu Glu Val Asp Ile Pro Arg Cys His Gln Tyr His  
 50 55 60  
 Pro Leu Leu Asn Ser Pro Ser Gly Ser Ala Gln Leu Arg Arg Ile Leu  
 65 70 75 80  
 Lys Ala Trp Gln Ile Val Tyr Leu Arg Pro Glu His Val Tyr Trp Gln  
 85 90 95  
 Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Thr Val Asn Asn Arg Asp  
 100 105 110  
 Glu Ala Leu Ala Phe Ala Gln Leu Asn Ala Phe Val Asn Arg Tyr Ile  
 115 120 125  
 His Trp Phe Tyr Leu Lys Asp Asn Ser Glu Val Ile Lys Glu Tyr Leu  
 130 135 140  
 Gly Lys Phe Tyr His Leu Thr Ala Tyr His Asp Pro Leu Leu Tyr Gln  
 145 150 155 160  
 His Leu Lys Ile Asn Gly Phe Asp Pro Glu  
 165 170

<210> 20  
 <211> 174  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 20

Asn Gly Leu Pro Leu Thr Pro Pro Ala Lys Gln Met Leu Gly Arg Phe  
1 5 10 15  
Pro Tyr Leu Gln Glu Leu Gln His Asp His Leu Cys Gln Tyr Leu His  
20 25 30  
Phe Ile Arg Gly Lys His Glu Arg Asp Leu Thr Ile Val Val Met Glu  
35 40 45  
His Tyr Gly Met Asn Leu Glu Asp Tyr Ala Lys Arg His Pro Pro Lys  
50 55 60  
Asp Glu Ala Gln Asn Asn Asn Phe Tyr Tyr Gln Ile Ala Cys Gly Ile  
65 70 75 80  
Asn Tyr Leu His Arg His His Ile Val His His Asn Leu His Pro Asn  
85 90 95  
His Ile Tyr Ile Thr Asp Asp Gly Asn Arg Lys Leu Ser Val Lys Leu  
100 105 110  
Phe Asn Tyr Gly Leu His His Met Thr Asn Tyr Gly Lys Tyr Thr Pro  
115 120 125  
Phe Pro Ile Gly Asn Gly Arg Tyr Met Ala Pro Glu Arg Ile Leu Asn  
130 135 140  
Asp Asn Asp Asn Leu Phe Ala Ala Thr Tyr Gln Ser Asp Val Trp Glu  
145 150 155 160  
Leu Gly Phe Ile Met Leu Gln Ile Tyr Leu Gly Ile Glu Leu  
165 170

<210> 21

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 21

Leu Ser Gln Ile Tyr His Leu Trp Gln Leu Ala Gly Gly Asp Val Gln  
1 5 10 15  
Ala Glu Leu Lys Lys Glu Gly Leu Ile Arg Ser Glu Ala Pro Ile Leu  
20 25 30  
Gly Leu Pro Gln Ile Val Arg Leu Ser Gly Ala Ser Val Cys Pro Gly  
35 40 45  
Arg Ser Gln Ala Gln Leu Met Asp Asp Arg Val Val Pro Leu Arg Leu  
50 55 60  
Lys Ala Leu Leu Gln Arg Leu Ser Gly Leu Pro Ala Ala Val Tyr Phe  
65 70 75 80  
Pro Leu Leu His Ser Pro Arg Phe Pro Ala His Phe Ala Arg Glu Leu  
85 90 95  
Gln Glu Leu Pro Leu Val Ile Arg Glu Lys Asp Ile Glu Tyr Gln Phe  
100 105 110  
Gln Arg Val Arg Leu Phe Ala Arg Leu Leu Gln Gly Tyr Pro His Thr  
115 120 125  
Ala Glu Gln  
130

<210> 22

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 22

Leu Lys Leu Ser Asn Val Val Arg Lys Ile Leu Ala Phe Gly Lys Ser  
1 5 10 15  
Asn Gly Ala Leu Glu Lys Ile Ala Arg Glu His Gln Cys His Glu Arg  
20 25 30  
Tyr Val Gln Met Asp Gln Arg Leu Arg Gln Leu Leu Glu Ser Cys Leu  
35 40 45  
Ser Val Leu Pro Lys Arg Arg Pro Leu Pro Gly Glu Leu Leu Glu His  
50 55 60  
Pro Ile Phe Glu Glu Val  
65 70

<210> 23

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 23

Pro Leu Ser Gln Ile Tyr His Leu Trp  
1 5

<210> 24

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 24

Leu Tyr Ala Phe Gln Trp Phe Leu Thr Leu Phe Ala Arg Glu Leu Pro  
1 5 10 15  
Leu Glu Thr Val Leu Arg Ile Trp Asp Cys Phe Phe Tyr Glu Gly Ser  
20 25 30  
Lys Ile Leu Phe Arg Val Ala Leu Ala Leu Leu Lys Met His Lys Glu  
35 40 45  
Glu Leu Leu Gln Ala Asp Asp Phe Glu Glu Met Leu Glu Phe Leu Gln  
50 55 60  
Asn Met Leu Pro Lys Arg Tyr Arg Ser Glu Glu Asp Ala Arg Arg Leu  
65 70 75 80  
Leu Glu Glu Ala Cys Asn Ile  
85

<210> 25

<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Met | Met | Glu | Lys | Leu | Gln | Lys | Gln | Ser | Met | Ser | Glu | Lys | Lys | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Glu | Glu | Met | Ser | Trp | Val | Ser | Gln | Leu | Met | Lys | Ile | Ala | Tyr | Gln | Ile |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ala | Lys | Gly | Leu | Glu | Tyr | Leu | His | Ser | Lys | Ser | Asn | Lys | Gln | Asn | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | His | Arg | Asp | Leu | Lys | Pro | Glu | Asn | Ile | Leu | Leu | Asp | Asn | Asn | Met |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Ala | Lys | Gly | Asp | Ser | Glu | Ile | Lys | Val | Val | Lys | Ile | Ala | Asp | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Gly | Leu | Ala | Arg | Met |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

<210> 26

<211> 133

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 26

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Thr | Pro | Ser | Tyr | Val | Lys | Tyr | Val | Gly | Thr | Arg | Trp | Tyr | Met | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Pro | Glu | Val | Leu | Met | Gly | Ser | Ser | Tyr | Gly | Gln | Tyr | Ser | Glu | Lys | Ser |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Val | Trp | Ser | Phe | Gly | Val | Ile | Leu | Tyr | Glu | Leu | Leu | Thr | Gly | Lys |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Pro | Phe | Phe | Pro | Gly | Ser | Ser | Glu | Val | Asn | Asp | Ser | Gln | Met | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Ile | Met | Lys | Glu | Thr | Met | Val | Lys | Ser | Ala | Glu | Tyr | Glu | Met | Pro |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Met | Lys | Met | Pro | Met | Pro | Glu | Ser | Ser | Lys | Glu | Ser | Met | Ser | Cys | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ser | Met | Ser | Ser | Glu | Ala | Val | Lys | Asp | Leu | Ile | Lys | Lys | Cys | Trp | Gln |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Asp | Pro | Glu | Lys | Arg | Pro | Thr | Phe | Ala | Gln | Val | Val | Glu | Glu | Leu |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Ala | His | Glu | Ile |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 130 |     |     |     |     |     |     |     |     |     |     |     |

<210> 27

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 27

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Pro | Gln | Ala | Leu | Asp | Ile | Gly | Val | Ala | Asp | Val | Glu | Leu | Lys | His |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Gln | Gln | Glu | Gln | Cys | Pro | Arg | Ile | Ser | Ala | Lys | Asp | Val | Gln | Phe |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

Leu Leu Asp Asn Ser Pro Ala Glu Leu Ala Leu Ile Asp Leu Arg Ser  
           35                          40                          45  
 Val Val Glu Phe Gly Arg Val His Val Pro His Ser Ile Asn Ile Pro  
           50                          55                          60  
 Phe Ala Thr Val Gln Leu Gly Glu Gln Arg Leu Glu Ala Leu Gln Val  
           65                          70                          75                          80  
 Pro Gln Leu Glu Ala Gln Leu Arg Gly Lys Ile Val Val Cys Val Ser  
                           85                          90                          95  
 Asn Ile His Gln His Ser Val Glu Val Gly His Pro Leu Ala Gln Leu  
                           100                          105                          110  
 Lys

<210> 28  
 <211> 94  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 28  
 Cys Val Leu Glu Ser Gln Lys Met Tyr Glu Ala Thr Pro Lys Ser Ile  
   1                          5                          10                          15  
 Thr His Arg Gln His Ala Leu Arg Leu Gln Pro Pro Gln Ala Leu Asp  
                           20                          25                          30  
 Ile Gly Val Ala Asp Val Glu Leu Lys His Leu Gln Gln Glu Gln Cys  
                           35                          40                          45  
 Pro Arg Ile Ser Ala Lys Asp Val Gln Phe Leu Leu Asp Asn Ser Pro  
                           50                          55                          60  
 Ala Glu Leu Ala Leu Ile Asp Leu Arg Ser Val Val Glu Phe Gly Arg  
                           65                          70                          75                          80  
 Val His Val Pro His Ser Ile Asn Ile Pro Phe Ala Thr Val  
                           85                          90

<210> 29  
 <211> 35  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Consensus amino acid sequence

<400> 29  
 Ser Gln Phe Ser His Phe Leu Val Ala Cys Gly Val Gln Arg Thr Cys  
   1                          5                          10                          15  
 Ile Leu His Lys Gly Phe Asn Val Leu His Ser Ile Glu Pro Asn Ile  
                           20                          25                          30  
 Leu Ile Ser  
                           35

<210> 30  
 <211> 148  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 30

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Asp Thr Asp Ile Gly Gly Cys Phe Glu Tyr Asn Thr Phe Pro Pro Pro
1           5           10           15
Gly Lys Tyr Tyr Arg Gly Lys Leu Gly Leu Glu Glu Tyr Ala Val Phe
20           25           30
Tyr Pro Pro Asn Gly Val Ile Pro Phe His Gly Phe Cys Met Tyr Ala
35           40           45
Ala Pro Phe Cys Tyr Leu Tyr His Glu Pro Ser Lys Leu Tyr Tyr Thr
50           55           60
Phe Arg Glu Phe Tyr Ile Arg Tyr Cys His Arg Leu His Thr Ile Asn
65           70           75           80
Thr His Pro Gln Gly Ile Val Ser Leu Cys Leu Leu Phe Glu Lys Leu
85           90           95
Leu Gln Thr Tyr Glu Pro Gln Leu Trp Tyr His Phe Arg Glu Ile Gly
100          105          110
Ala Gln Pro Leu Arg Ile Ser Phe Lys Trp Met Met Arg Ala Phe Ser
115          120          125
Gly His Leu Pro Pro Asp Gln Leu Leu Leu Leu Trp Asp Arg Ile Leu
130          135          140
Gly Tyr Asn Ser
145

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<210> 31

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 31

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Ser Ala Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu
1           5           10           15
Thr Leu Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr
20           25           30
Leu His Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile
35           40           45
Leu Ile Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu
50           55           60
His Ser Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe
65           70           75           80
Pro Gln Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu
85           90           95
Arg Gln Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val
100          105          110
Gly Ile Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp
115          120          125
Met His Arg Thr Gln Met Leu
130          135

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<210> 32

<211> 37

<212> PRT

<213> Artificial Sequence



<220>

<223> Consensus amino acid sequence

<400> 32

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Phe | Ser | Pro | Ala | Phe | Phe | Ser | Leu | Val | Gln | Leu | Cys | Leu | Gln |
| 1   |     |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Asp | Pro | Glu | Lys | Arg | Pro | Ser | Ala | Ser | Ser | Leu | Leu | Ser | His | Val |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Phe | Phe | Lys | Gln | Met |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 33

<211> 101

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 33

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Phe | Arg | Leu | Leu | Leu | Gln | Tyr | His | Asp | Pro | Glu | Leu | Cys | Asn | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Asp | Thr | Lys | Lys | Cys | Thr | Pro | Asp | Met | Tyr | Thr | Leu | Asn | Trp | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ser | Leu | Phe | Ala | Ser | Cys | Cys | Ser | Thr | Glu | Val | Cys | His | Ala | Leu |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Trp | Asp | Leu | Tyr | Ile | Gln | Gln | Ala | Asp | Pro | Phe | Met | Val | Phe | Phe | Leu |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Leu | Ile | Ile | Leu | Ile | Asn | Ala | Lys | Glu | Glu | Ile | Leu | Gln | Met | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Asp | Ser | Lys | Glu | Glu | Val | Ile | Lys | Phe | Leu | Glu | Asn | Met | Pro | Cys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Gln | Leu | Asn | Ile | Glu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 34

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 34

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Val | Asp | Cys | Arg | Pro | Ala | Glu | Gln | Tyr | Asn | Ala | Gly | His | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ala | Phe | His | Leu |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 35

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 35  
 Val Ile His Arg Asn Ile Cys Pro Glu Ser Ile Leu Ile Thr Lys Arg  
 1 5 10 15  
 Gly Ser Trp Lys Leu Ala Gly Phe Asp Phe Cys Val Ser Ala Gln Asn  
 20 25 30  
 Pro Asn Asp Gln Glu Asn Tyr Phe Pro Cys His Tyr Glu Trp Asp Pro  
 35 40 45  
 Arg Ile Pro Pro Leu Pro Leu Gln Pro Asn Leu Asp Tyr Leu Ala Pro  
 50 55 60  
 Glu Tyr Val Thr Ser Ser Thr Cys Thr Val Gly Ser Ala Ser Asp Met  
 65 70 75 80  
 Phe Ser Leu Gly Cys Leu Ile Tyr Ala Ile Tyr Asn Gly Gly Lys Pro  
 85 90 95  
 Leu Ile Asp Ala Asn Asn Asn Asp Glu Tyr Lys Ser Asn Tyr Asn Lys  
 100 105 110  
 Tyr Met Asn Thr Leu Asn Ser Leu Thr His Glu Ser Met Asn Asn Leu  
 115 120 125  
 Pro Pro Glu Asn Leu Lys Glu Ser Leu Lys Arg Met Leu Ser Met Asp  
 130 135 140  
 Pro Thr Val Arg Pro Thr Ala Gln Glu Leu Thr Leu Ile Lys Tyr Phe  
 145 150 155 160

<210> 36

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 36

Asp Leu Leu Leu Gln Lys Thr Pro Pro Glu Asp Ile Lys Ser Asn Ile  
 1 5 10 15  
 Leu Pro Met Leu Tyr Tyr Ala Phe Glu Asp Ser Asp Ile Gln Ile Cys  
 20 25 30  
 Gln

<210> 37

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<221> VARIANT

<222> (1)...(261)

<223> Xaa = Any Amino Acid

<400> 37

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Gly Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45

cont  
A1

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
85 90 95  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa  
100 105 110  
Xaa Xaa Xaa Xaa His Arg Asp Xaa Lys Xaa Xaa Asn Xaa Xaa Xaa Xaa  
115 120 125  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
130 135 140  
Asp Phe Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
145 150 155 160  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa  
165 170 175  
Xaa Xaa Xaa Xaa Xaa Xaa Trp Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa  
180 185 190  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
195 200 205  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
210 215 220  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
225 230 235 240  
Xaa Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
245 250 255  
Xaa His Xaa Xaa Xaa  
260

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